Amendments to the Specification

At page 8, line 18, please amend the paragraph as follows:

Unless otherwise stated, sequence identity/similarity values provided herein refer to the value obtained using the BLAST 2.0 suite of programs using default parameters. Altschul et al., *Nucleic Acids Res.* 25:3389-3402 (1997). Software for performing BLAST analyses is publicly available, e.g., through the National Center for Biotechnology-Information at worldwide web at ~~(http://www.~~ncbi.nlm.nih.gov/~~)~~.

At page 11, line 24, please amend the paragraph as follows:

As used herein, often the designation of a particular polymorphism is made by the name of a particular restriction enzyme. This is not intended to imply that the only way that the site can be identified is by the use of that restriction enzyme. There are numerous databases and resources available to those of skill in the art to identify other restriction enzymes which can be used to identify a particular polymorphism. Two examples are: worldwide web at ~~http://www.~~geneseo.edu/~bio/ and worldwide web at ~~http://www.~~firstmarket.com/cutter/cut2~~.html~~. In fact, as disclosed in the teachings herein there are numerous ways of identifying a particular polymorphism or allele with alternate methods which may not even include a restriction enzyme, but which assay for the same genetic or proteomic alternative form.

At page 30, line 15, please amend the paragraph as follows:

Although the methods described herein may be in terms of the use of a single restriction enzyme and a single set of primers, the methods are not so limited. One or more additional restriction enzymes and/or probes and/or primers can be used, if desired. Indeed in some situations it may be preferable to use combinations of markers giving specific haplotypes. Additional enzymes, constructed probes and primers can be determined through routine experimentation, combined with the teachings provided and incorporated herein. Stand alone software as well as web-based software are avaible that allows the user to identify other restriction mapping sites in the DNA sequence, e.g., worldwide web at ~~http://www.~~restrictionmapper.org/.

At page 38, line 23, please amend the paragraph as follows:

Conformation of genotype frequencies to Hardy-Weinberg equilibrium was tested using the GENEPOP computer package at worldwide web ~~(http://~~wbiomed.curtin.edu.au/genepop~~)~~ using the default options (1000 dememorisation, 100 batches and 1000 iterations). The program uses the Markov chain method to estimate the exact Hardy-Weinberg probability without bias (Guo and Thompson, 1992). The probability of rejecting H_o, i.e., genotype frequencies are in Hardy-Weinberg equilibrium and the standard error of this estimate were computed. When standard errors were larger than 0.01, the data were re-analysed using a larger number of batches. This program does not perform any test when a locus is monomorphic or quasi monomorphic (two alleles, but one is represented only once).